RESPONSE

I. Status of the Claims

Claims 5 and 6 have been added. Claims 2-6 are therefore presently pending in the case.

II. Support for the Amended Claims

Claims 5 and 6 have been added. New Claim 5 has been added to more clearly claim the invention and finds support throughout the specification as originally filed with particular support being provided at least on page 11, lines 9-16. New Claim 6 has also been added to more clearly claim the invention and finds support throughout the specification as originally filed with particular support being provided at least on page 11, lines 16-26. As new claims 5 and 6 are supported by the specification and claims as originally filed, they do not constitute new matter and entry therefore is respectfully requested.

III. Rejection of Claims Under 35 U.S.C. § 101

Rejection of Claims 2-4 under 35 U.S.C. § 101 because the claimed invention allegedly lacks patentable utility is maintained. The Examiner's rejection is respectfully traversed, based on the following arguments as well as those presented in earlier responses.

The rejection of Claims 2-4 is maintained in this Final Action which again asserts that Applicants have failed to identify the function of the protein encoded by the sequences of the present invention and that therefore there can be no specific, substantial or credible utility "Since the specification sets forth no specific function for the encoded protein, the claimed polynucleotides encode a protein with no ascribe function" (page 3 lines 21-22).

That this issue remains is difficult to believe, given the fact that the disclosure in the specification which repeatedly describes the molecules of the present invention as a novel human kinase as do many of the claims. In addition, Applicants' previous responses, which clearly reiterate Applicants' position and assertion that the molecules of the present invention encode a human kinase with all the utility that is well-recognized by the art.

Previous Actions noted that Applicant has argued that the polypeptide of SEQ ID NO:2 is a kinase by citing Published PCT Applications of others (WO 01/66594 and WO 02/10401). Applicants' intent was to demonstrate that Applicants' assertion that the sequences of the present invention encode a kinase is credible. Clearly when faced with the same information, those of skill in the art, whom are independent and in no was associated with Applicants, also identified the molecules of the present invention as a kinase. Thus, clearly Applicants' assertion that the sequences of the present invention encode a kinase is credible. As the legal test for utility simply involves an assessment of whether those skilled in the art would find any of the utilities described for the invention to be credible or believable. Clearly those of skill in the art would recognize that molecules that share nucleic acid sequence identity would share protein structure and would thus also share function. This evidence clearly supports the specifications assertion that SEQ ID NO:1 and 2 encode a protein kinase.

The Final Action dismisses Applicants' continued assertions that the protein of the present invention is a protein kinase and that as a kinase protein their function is both well known and implied to those of skill in the art. A protein kinase is known to those of skill in the art to be an enzyme that phosphorylates proteins by transferring a phosphate group from a purine triphosphate such as ATP. More specifically, serine/threonine kinases are protein kinases that phosphorylate serine and threonine residues. This is the well-established function of kinase proteins.

In addition, the Final Action states that "mere homology of SEQ ID No:1 to a known DNA molecule with a known function does not endow SEQ ID NO:1 with the function because SEQ ID NO:1 could also be a DNA molecule encoding a protein of a different function" (Page 3, lines 7-9). Applicants now understand that the Examiners' earlier declaration that the sequences of the present invention are a Rab GTPase (paper no 18 at page 5, lines 4-6) "If one were to follow the applicant's line of reasoning, SEQ ID NO:1 could be identified as a Rab GTPase" as SEQ ID NO:1 it is 99.2% identical to a Rab GTPase was merely an example that the Examiner synthesized to make a point. Applicants' misunderstanding and confusion stemmed in part from Applicants' knowledge that most protein kinases are involved in a network of autophosphorylation and phosphorylaion by other kinases and that the protein encoded by the sequences of the present invention contains a RabGAP/TBC domain which is indicative of the interaction of this protein kinase with Rab-like GTPases. Regardless, Applicants' position remains as stated previously in the Response to the Action of Paper No. 18 (Paper No. 19), that it is logical to assume that if a polynucleotide is 99.2% identical to a known

polynucleotide, whose function has been identified that the heretofore unknown polynucleotide encodes a slight variant or isoform of the known molecule with a similar function and that such information would clearly support the credibility of Applicants' assertion.

The Examiner's statement that "mere homology of SEQ ID No:1 to a known DNA molecule with a known function does not endow SEQ ID NO:1 with the function because SEQ ID NO:1 could also be a DNA molecule encoding a protein of a different function" (Page 3, lines 7-9) is contrary to Example 10 of the PTO's Revised Interim Utility Guidelines Training Materials (pages 53-55), which establishes that a rejection under 35 U.S.C. § 101 as allegedly lacking a patentable utility and under 35 U.S.C. § 112, first paragraph as allegedly unusable by the skilled artisan due to the alleged lack of patentable utility, is not proper when there is no reason to doubt the asserted utility of a full length sequence (such as the presently claimed sequence) that has a similarity score of 95% to a protein having a known function. In the Analysis portion of Example 10 it states that "Based on applicant's disclosure and the results of the PTO search, there is no reason to doubt the assertion that SEQ ID NO:2 encodes a DNA ligase. Further DNA ligases have a well-established use in the molecular biology art based on this class of proteins ability to ligate DNA. .....Note that if there is a well-established utility already associated with the claimed invention, the utility need not be asserted in the specification as filed..... Thus the conclusion reached from this analysis is that a 35 U.S.C. § 101 and a 35 U.S.C. § 112 first paragraph, utility rejection should not be made."

The present case is the same as that presented in Example 10 of the Revised Interim Utility Guidelines Training Materials (pages 53-55). In the present case it is clear that the sequences of the present invention encode a protein kinase. Protein kinases have a well-established use in the molecular biology art based on this class of proteins ability to phosphorylate proteins at serine and threonine residues, (this utility is so well known that U.S. Patent No. 5,817,479 has issued on human kinase fragments). Thus a 35 U.S.C. § 101 and a 35 U.S.C. § 112 first paragraph, utility rejection should not have been made and should be withdrawn.

Furthermore, the Final Action questions the existence of the proteins encoded by the sequences of the present invention

due to the lack of examples that provide "objective evidence".

However, it has long been established that "there is no statutory requirement for the disclosure of a specific example". *In re Gay*, 135 USPQ 311 (C.C.P.A. 1962). Applicants assertion of the

stated utility is legally sufficient and should control the utility analysis unless the Examiner meets the burden of establishing the lack of utility by making evidence of record that conclusively refutes the Applicants asserted utility. This principle is affirmed in Example 10 of the PTO's Revised Interim Utility Guidelines Training Materials (pages 53-55) when phrases such as "there is no reason to doubt the assertion" and "Note that if there is a well-established utility already associated with the claimed invention, the utility need not be asserted in the specification as filed".

However, the fact is that "evidence" for the existence of the protein, encoded by the sequences of the present invention, has been presented. For example, the specification as filed provided tissue specific expression information in the first paragraph of Section 5 (page 3) "a novel protein that is expressed in, *inter alia,* human cell lines, and human brain, pituitary, cerebellum, spinal cord, thymus, lymph node, bone marrow, trachea, kidney, liver, prostate, testis, thyroid, adrenal gland, pancreas, stomach, small intestine, colon, skeletal muscle, uterus, placenta, mammary gland, adipose, esophagus, bladder, cervix, rectum, pericardium, hypothalamus, ovary, fetal kidney, and fetal lung cells".

When Applicants provided additional "evidence" regarding the existence and activity of the protein, encoded by the sequences of the present invention, in the form of additional information Applicants had obtained by generating knockout mice lacking the murine homolog of the claimed polynucleotide (in Paper 19) the Examiner' responded by alleging that "The specification does not contain such experiments" (Final Action at page 3 line 17).

Applicants respectfully disagree, for while the results of the analysis of knockout mice was not described in the specification as filed, the generation of knockout mice was. The specification as originally filed clearly states that "The present invention also includes both transgenic animals that express a NHP transgene, and NHP "knock-outs" (which can be conditional) that do not express a functional NHP." (specification at page 2, lines 22-25). Thus, the broad class of knockout animals, which by definition includes knockout mice, lacking the orthologous sequence that corresponds to the claimed sequence are clearly supported by the specification as originally filed.

Clearly, Applicants' description of the physiologic effect that disrupting the murine homolog of the claimed polynucleotide in knockout mice, provides "objective evidence" that said protein exists and has physiologic function.

As set forth in *In re Langer* (183 USPQ 288 (CCPA 1974); "*Langer*"):

> As a matter of Patent Office practice, a specification which contains a disclosure of utility which corresponds in scope to the subject matter sought to be patented must be taken as sufficient to satisfy the utility requirement of § 101 for the entire claimed subject matter unless there is a reason for one skilled in the art to question the objective truth of the statement of utility or its scope.

Langer at 297, emphasis in original. As set forth in the MPEP, "Office personnel must provide evidence sufficient to show that the statement of asserted utility would be considered 'false' by a person of ordinary skill in the art" (MPEP, Eighth Edition at 2100-40, emphasis added). Thus, absent such evidence from the Examiner concerning the role of the presently claimed sequence encodes a protein kinase, the present claims clearly meet the requirements of 35 U.S.C. § 101.

An additional utility includes the use of the presently claimed polynucleotides on DNA chips. Further, the Action seems to be requiring Applicants to identify the biological role of the nucleic acid or function of the protein encoded by the presently claimed polynucleotides before the present sequences can be used in gene chip applications that meet the requirements of § 101. Applicants respectfully point out that knowledge of the exact function or role of the presently claimed sequence is not required to track expression patterns using a DNA chip. Given the widespread utility of such "gene chip" methods using *public domain* gene sequence information, there can be little doubt that the use of the presently described *novel* sequences would have great utility in such DNA chip applications. The claimed sequence provides a specific marker of the human genome (see evidence below), and that such specific markers are targets for discovering drugs that are associated with human disease. Thus, those skilled in the art would instantly recognize that the present nucleotide sequence would be an ideal, novel candidate for assessing gene expression using, for example, DNA chips, as the specification details. Such "DNA chips" clearly have utility, as evidenced by hundreds of issued U.S. Patents, as exemplified by U.S. Patent Nos. 5,445,934, 5,556,752, 5,744,305, as well as more recently issued U.S. Patent Nos. 5,837,832, 6,156,501 and 6,261,776. Accordingly, the present sequence has a specific utility in such DNA chip applications. Clearly, compositions that enhance the utility of such DNA chips, such as the presently claimed nucleotide sequence, must also be useful.

Additionally, since only a small percentage of the genome (2-4%) actually encodes exons, which in-turn encode amino acid sequences. Thus, not all human genomic DNA sequences are useful in such gene chip applications. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101. It has been clearly established that a statement of utility in a specification must be accepted absent

reasons why one skilled in the art would have reason to doubt the objective truth of such statement. *In re Langer*, 503 F.2d 1380, 1391, 183 USPQ 288, 297 (CCPA, 1974); *In re Marzocchi*, 439 F.2d 220, 224, 169 USPQ 367, 370 (CCPA, 1971).

Evidence of the "real world" substantial utility of the present invention is further provided by the fact that there is an entire industry established based on the use of gene sequences or fragments thereof in a gene chip format. Perhaps the most notable gene chip company is Affymetrix. However, there are many companies which have, at one time or another, concentrated on the use of gene sequences or fragments, in gene chip and non-gene chip formats, for example: Gene Logic, ABI-Perkin-Elmer, HySeq and Incyte. In addition, one such company, Rosetta Inpharmatics, was viewed to have such "real world" value that it was acquired by large pharmaceutical company, Merck & Co., for substantial sums of money (net equity value of the transaction was $620 million). The "real world" substantial industrial utility of gene sequences or fragments would, therefore, appear to be widespread and well established. Clearly, persons of skill in the art, as well as venture capitalists and investors, readily recognize the utility, both scientific and commercial, of genomic data in general, and specifically human genomic data. Billions of dollars have been invested in the human genome project, resulting in useful genomic data (see, *e.g.*, Venter *et al.*, 2001, Science *291*:1304). The results have been a stunning success as the utility of human genomic data has been widely recognized as a great gift to humanity (see, *e.g.*, Jasny and Kennedy, 2001, Science *291*:1153). Clearly, the usefulness of human genomic data, such as the presently claimed nucleic acid molecules, is substantial and credible (worthy of billions of dollars and the creation of numerous companies focused on such information) and well-established (the utility of human genomic information has been clearly understood for many years). Given the physiologic effects observed following disruption of the mouse homolog of the protein encoded by the claimed sequences, those of skill in the art would readily appreciate the importance of tracking the expression of the genes encoding the described proteins, particularly due to well established role of protein kinases in cell growth regulation, cancer and other diseases. The use of the claimed polypeptide in an array for screening purposes Applicants respectfully point out that nucleic acid sequences have the greatest specific utility in gene chip applications once the role of the sequence has been identified, as have tissues of interest, as in the present case. Once the role of the particular nucleic acid is known, the level of gene expression has and even greater significance. By identifying the physiological activity role of the claimed sequence, the claimed sequence has a far greater utility in gene chip applications that

just any random piece of DNA. Applicants respectfully submit that **specific** utility, which is the proper standard for utility under 35 U.S.C. § 101, is distinct from the requirement for a **unique** utility, which is clearly an improper standard. As clearly stated by the Federal Circuit in *Carl Zeiss Stiftung v. Renishaw PLC*, 20 USPQ2d 1101 (Fed. Cir. 1991; "*Carl Zeiss*"):

> An invention need not be the best or only way to accomplish a certain result, and it need only be useful to some extent and in certain applications: "[T]he fact that an invention has only limited utility and is only operable in certain applications is not grounds for finding a lack of utility." *Envirotech Corp. v. Al George, Inc.*, 221 USPQ 473, 480 (Fed. Cir. 1984)

Therefore, just because other nucleic acid sequences find utility in gene chip applications does not mean that the use of Applicants' sequence in gene chip applications is not a specific utility. Furthermore, the requirement for a unique utility is clearly not the standard adopted by the Patent and Trademark Office. If every invention were required to have a unique utility, the Patent and Trademark Office would no longer be issuing patents on batteries, automobile tires, golf balls, golf clubs, and treatments for a variety of human diseases, such as cancer and bacterial or viral infections, just to name a few particular examples, because examples of each of these have already been described and patented. All batteries have the exact same utility - specifically, to provide power. All automobile tires have the exact same utility - specifically, for use on automobiles. All golf balls and golf clubs have the exact same utility - specifically, use in the game of golf. All cancer treatments have the exact same utility - specifically, to treat cancer. All anti-infectious agents have the exact same broader utility - specifically, to treat infections. However, only the briefest perusal of virtually any issue of the Official Gazette provides numerous examples of patents being granted on each of the above compositions every week. Furthermore, if a composition needed to be unique to be patented, the entire class and subclass system would be an effort in futility, as the class and subclass system serves solely to group such common inventions, which would not be required if each invention needed to have a unique utility. Thus, the present sequence clearly meets the requirements of 35 U.S.C. § 101.

Although Applicants need only make one credible assertion of utility to meet the requirements of 35 U.S.C. § 101 (*Raytheon v. Roper*, 220 USPQ 592 (Fed. Cir. 1983); *In re Gottlieb*, 140 USPQ 665 (CCPA 1964); *In re Malachowski*, 189 USPQ 432 (CCPA 1976); *Hoffman v. Klaus*, 9 USPQ2d 1657 (Bd. Pat. App. & Inter. 1988)), as a further example of the utility of the presently claimed polynucleotides, as described in the specification at least at page 8 line 13, the present

nucleotide sequence has a specific utility in determining the genomic structure of the corresponding human chromosome, for example mapping the protein encoding regions. As evidence supporting Applicants assertions of the specific utility of the sequences of the present invention in localizing the specific region of the human chromosome and identification of functionally active intron/exon splice junctions is the information provided as **Exhibit A**. This is the result of overlaying the sequence of SEQ ID NO:1 of the present invention and the identified human genomic sequence. By doing this, one is able to identify the portions of the genome that encode the present invention. As these regions of the genome are non-contiguous, this is indicative of individual exons. The results of such an analysis indicate that the sequence of the present invention is the result of a 25 exon gene contained within the BAC clones AC09360.2, AC107381.2, Sc114734.4, AP001820.2 and AC109361.4. Clearly as the gene of the present invention is encoded by 25 non-contiguous exons on chromosome 4, one would not have been able to deduce the sequence that encodes the molecules of the present invention without knowing the sequence. Clearly, the present polynucleotide provides exquisite specificity in localizing the specific region of human chromosome 4 that contains the gene encoding the given polynucleotide, a utility not shared by virtually any other nucleic acid sequences. In fact, it is this specificity that makes this particular sequence so useful. Early gene mapping techniques relied on methods such as Giemsa staining to identify regions of chromosomes. However, such techniques produced genetic maps with a resolution of only 5 to 10 megabases, far too low to be of much help in identifying specific genes involved in disease. The skilled artisan readily appreciates the significant benefit afforded by markers that map a specific locus of the human genome, such as the present nucleic acid sequence. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Equally significant is that the claimed polynucleotide sequences define how the encoded exons are actually spliced together to produce an active transcript (*i.e.*, the described sequences are useful for functionally defining exon splice-junctions). The presently claimed sequence clearly identified the intron/exon boundaries, as described above. The specification details that "sequences derived from regions adjacent to the intron/exon boundaries of the human gene can be used to design primers for use in amplification assays to detect mutations within the exons, introns, splice sites (*e.g.*, splice acceptor and/or donor sites), *etc.*, that can be used in diagnostics and pharmacogenomics" (specification at page 8, lines 14-20). Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Applicants again draw attention to the distinction between the requirements of a specific utility with a unique utility. The fact that a small number of other nucleotide sequences could be used to map the protein coding regions in this specific region of chromosome 4 does not mean that the use of Applicants' sequence to map the protein coding regions of chromosome 4 is not a specific utility (*Carl Zeiss Stiftung v. Renishaw PLC, supra*).

Finally, while Applicants are well aware of the new Utility Guidelines set forth by the USPTO, it has been long established that the current rules regarding the examination of patent applications is and always has been the patent laws as set forth in 35 U.S.C. and the patent rules as set forth in 37 C.F.R., not the Manual of Patent Examination Procedure or particular guidelines for patent examination set forth by the USPTO. Furthermore, it is the job of the judiciary, not the USPTO, to interpret these laws and rules. Applicants point out that guidelines that are not consistent with the patent laws, or the interpretation of these laws by the judicial branch, are not the final word in determining whether or not claims comply with any particular section of the patent laws. Applicants are unaware of any significant recent changes in either 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit that is in keeping with the new Utility Guidelines set forth by the USPTO. This is underscored by numerous patents that have been issued over the years that claim nucleic acid fragments that do not comply with the new Utility Guidelines. As examples of such issued U.S. Patents, the Examiner is invited to review U.S. Patent Nos. 5,817,479, 5,654,173, and 5,552,281 (each of which claim short polynucleotides), none of which contain examples of the "real-world" utilities that seem to be required in the Action. As issued U.S. Patents are presumed to meet all of the requirements for patentability, including 35 U.S.C. §§ 101 and 112, first paragraph (see Section III, below), Applicants submit that the presently claimed polynucleotides must also meet the requirements of 35 U.S.C. § 101. While Applicants understand that each patent application is examined on the basis of its individual merits, Applicants are unaware of any changes to 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit, since the issuance of these patents that render the subject matter claimed in these patents, which is similar to the subject matter in question in the present application, as suddenly non-statutory or failing to meet the requirements of 35 U.S.C. § 101. The requirement of Applicants to meet a different standard of utility in the present case would be arbitrary and capricious, and cannot stand.

In summary, the present situation directly tracks Example 10 of the Revised Interim Utility Guidelines Training Materials (pages 53-55), which establishes that a rejection under 35 U.S.C. § 101 as allegedly lacking a patentable utility and under 35 U.S.C. § 112, first paragraph as allegedly unusable by the skilled artisan due to the alleged lack of patentable utility, is not proper when the full length sequence of the invention encodes a protein that has a well known function. Furthermore this response has described a series of additional substantial, specific, credible and well-established utilities for the present invention in addition to those described in Applicants' many previous responses. Therefore, Applicants submit that as the presently claimed sequence molecules have been shown to have a substantial, specific, credible and well-established utility, the rejection of the claims under 35 U.S.C. § 101 has been overcome. Thus, Applicants respectfully request that the rejection be withdrawn.

IV. Rejection of Claims Under 35 U.S.C. § 112, First Paragraph

The rejection of the Claims 2-4 under 35 U.S.C. § 112 first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention due to an alleged lack of utility is also maintained.

Applicants respectfully submit that Claims 2-4 have been shown to have "a specific, substantial, and credible utility", as detailed in the section above. Therefore, one skilled in the art would clearly know how to use the claimed invention and Applicants therefore request that the rejection of claims. Therefore, Applicants submit that as the presently claimed sequence molecules have been shown to have a substantial, specific, credible and well-established utility, and thus the rejection of the claims under 35 U.S.C. § 112, first paragraph has been avoided. Thus, Applicants respectfully request that the rejection be withdrawn.

V. Conclusion

The present document is a full and complete response to the Action. In conclusion, Applicants submit that, in light of the foregoing remarks, the present case is in condition for allowance, and such favorable action is respectfully requested. Should Examiner Pak have any questions or comments, or

believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

September 8, 2003
Date

Lance K. Ishimoto Reg. No. 41,866

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MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.fa
26,679 sequences; 200,800,637,119 total letters

Query= LEX83seqid1
(2682 letters)

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 Score =  317 bits (160), Expect = 2e-83
 Identities = 160/160 (100%)
 Strand = Plus / Minus

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Sbjct: 24091 agaaggggagcttacccagggcccttacactgctatgctccagaacttcaaagggaaggt 24032

Query: 2532  cattgtcatcgtggggcatgtggcaaaacacacagctgag 2571
              |||||||||||||||||||||||||||||||||||||||
Sbjct: 24031 cattgtcatcgtggggcatgtggcaaaacacacagctgag 23992


>AC114734.4.1.78693
          Length = 78693

 Score =  321 bits (162), Expect = 1e-84
 Identities = 162/162 (100%)
 Strand = Plus / Minus

Query: 1898 atgtatttccactacacaaaattttccacctctgggataccttactacttgggaattcct 1957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1236 atgtatttccactacacaaaattttccacctctgggataccttactacttgggaattcct 1177

Query: 1958 ctttcccattctgtattggagtagcaattcttcagcagctgcgggaccggcttttggcta 2017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1176 ctttcccattctgtattggagtagcaattcttcagcagctgcgggaccggcttttggcta 1117

Query: 2018 atggctttaatgagtgtattcttctcttctccgatttaccag 2059
          |||||||||||||||||||||||||||||||||||||||||
Sbjct: 1116 atggctttaatgagtgtattcttctcttctccgatttaccag 1075
```

```
 Score =  291 bits (147), Expect = 1e-75
 Identities = 150/151 (99%)
 Strand = Plus / Minus

Query: 781   aggccaaccccagatgaattaatgaaggacaaagtattcagtgaggtatcacctttatat 840
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 54755 aggccaaccccagatcaattaatgaaggacaaagtattcagtgaggtatcacctttatat 54696

Query: 841   acccccttttaccaaacctgccagtctgttttcatcttctctgagatgtgctgatttaact 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 54695 acccccttttaccaaacctgccagtctgttttcatcttctctgagatgtgctgatttaact 54636

Query: 901   ctgcctgaggatatcagtcagttgtgtaaag 931
              |||||||||||||||||||||||||||||
Sbjct: 54635 ctgcctgaggatatcagtcagttgtgtaaag 54605


 Score =  285 bits (144), Expect = 7e-74
 Identities = 144/144 (100%)
 Strand = Plus / Minus

Query: 455   ggtatccctcgtacttggcccctgaggtaattgcacagggaattttcaaaaccactgatc 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59474 ggtatccctcgtacttggcccctgaggtaattgcacagggaattttcaaaaccactgatc 59415

Query: 515   acatgccaagtaaaaaaccattgccttctggccccaaatcagatgtatggtctcttggaa 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59414 acatgccaagtaaaaaaccattgccttctggccccaaatcagatgtatggtctcttggaa 59355

Query: 575   tcattttatttgagctttgtgtgg 598
              ||||||||||||||||||||||||
Sbjct: 59354 tcattttatttgagctttgtgtgg 59331


 Score =  280 bits (141), Expect = 4e-72
 Identities = 141/141 (100%)
 Strand = Plus / Minus

Query: 930   agatataaataatgattacctggcagaaagatctattgaagaagtgtattacctttggtg 989
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52232 agatataaataatgattacctggcagaaagatctattgaagaagtgtattacctttggtg 52173

Query: 990   tttggctggaggtgacttggagaaagagcttgtcaacaaggaaatcattcgatccaaacc 1049
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52172 tttggctggaggtgacttggagaaagagcttgtcaacaaggaaatcattcgatccaaacc 52113

Query: 1050  acctatctgcacactccccaa 1070
              |||||||||||||||||||||
```

```
Sbjct: 52112 acctatctgcacactccccaa 52092


 Score =  260 bits (131), Expect = 4e-66
 Identities = 131/131 (100%)
 Strand = Plus / Minus

Query: 1221  ccagtctaatttacctcattcaaacagcaataatgagttgtctgcagctgccacgctccc 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 43985 ccagtctaatttacctcattcaaacagcaataatgagttgtctgcagctgccacgctccc 43926

Query: 1281  tttaatcatcagagagaaggatacagagtaccaactaaatagaattattctcttcgacag 1340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 43925 tttaatcatcagagagaaggatacagagtaccaactaaatagaattattctcttcgacag 43866

Query: 1341  gctgctaaagg 1351
              ||||||||||||
Sbjct: 43865 gctgctaaagg 43855


 Score =  256 bits (129), Expect = 6e-65
 Identities = 129/129 (100%)
 Strand = Plus / Minus

Query: 1513  attgaagtggatattcctcgctgtcatcagtacgatgaactgttatcatcaccagaaggt 1572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 40530 attgaagtggatattcctcgctgtcatcagtacgatgaactgttatcatcaccagaaggt 40471

Query: 1573  catgcaaaatttaggcgtgtattaaaagcctgggtagtgtctcatcctgatcttgtgtat 1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 40470 catgcaaaatttaggcgtgtattaaaagcctgggtagtgtctcatcctgatcttgtgtat 40411

Query: 1633  tggcaaggt 1641
              |||||||||
Sbjct: 40410 tggcaaggt 40402


 Score =  234 bits (118), Expect = 2e-58
 Identities = 118/118 (100%)
 Strand = Plus / Minus

Query: 265   agctgttcaacggttttgtgtatagcatttgaggttcttcagggcttgcagtatatgaac 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 69680 agctgttcaacggttttgtgtatagcatttgaggttcttcagggcttgcagtatatgaac 69621

Query: 325   aaacatggtatagtacacagggcattgtctcctcataatatcctgttggaccgaaagg 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 69620 aaacatggtatagtacacagggcattgtctcctcataatatcctgttggaccgaaagg 69563
```

```
 Score =  202 bits (102), Expect = 8e-49
 Identities = 102/102 (100%)
 Strand = Plus / Minus

Query: 1349  aggcttatccatataaaaaaaaccaaatctggaaagaagcaagagttgacattcctcctc 1408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 42835 aggcttatccatataaaaaaaaccaaatctggaaagaagcaagagttgacattcctcctc 42776


Query: 1409  ttatgagaggtttaacctgggctgctcttctgggagttgagg 1450
              |||||||||||||||||||||||||||||||||||||||||
Sbjct: 42775 ttatgagaggtttaacctgggctgctcttctgggagttgagg 42734


 Score =  198 bits (100), Expect = 1e-47
 Identities = 100/100 (100%)
 Strand = Plus / Minus

Query: 1071  ttttctctttgaggatggtgaaagctttggacaaggtcgagatagaagctcgcttttaga 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50035 ttttctctttgaggatggtgaaagctttggacaaggtcgagatagaagctcgcttttaga 49976


Query: 1131  tgataccactgtgacattgtcgttatgccagctaagaaat 1170
              |||||||||||||||||||||||||||||||||||||||
Sbjct: 49975 tgataccactgtgacattgtcgttatgccagctaagaaat 49936


 Score =  174 bits (88), Expect = 2e-40
 Identities = 88/88 (100%)
 Strand = Plus / Minus

Query: 1773  agagtatctgactgtcttctctcagatgattgcatttcatgatccagagctgagtaatca 1832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20303 agagtatctgactgtcttctctcagatgattgcatttcatgatccagagctgagtaatca 20244


Query: 1833  tctcaatgagattggtttcattccagat 1860
              |||||||||||||||||||||||||||
Sbjct: 20243 tctcaatgagattggtttcattccagat 20216


 Score =  170 bits (86), Expect = 3e-39
 Identities = 86/86 (100%)
 Strand = Plus / Minus

Query: 1689  agccttggcttatgcatgtatgtctgcttttattcccaaatacctgtataacttcttctt 1748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 37914 agccttggcttatgcatgtatgtctgcttttattcccaaatacctgtataacttcttctt 37855
```

```
Query: 1749  aaaagacaactcacatgtaatacaag 1774
             |||||||||||||||||||||||||
Sbjct: 37854 aaaagacaactcacatgtaatacaag 37829
```

Score = 157 bits (79), Expect = 4e-35
Identities = 79/79 (100%)
Strand = Plus / Minus

```
Query: 380   agggacatattaaattggctaaatttggactttatcacatgacagctcatggtgatgatg 439
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 67978 agggacatattaaattggctaaatttggactttatcacatgacagctcatggtgatgatg 67919
```

4)

```
Query: 440   ttgatttcccaatagggta 458
              ||||||||||||||||||
Sbjct: 67918 ttgatttcccaatagggta 67900
```

Score = 129 bits (65), Expect = 1e-26
Identities = 65/65 (100%)
Strand = Plus / Minus

```
Query: 1448  agggagctattcatgccaagtacgatgcaattgataaagacactccaattcctacagata 1507
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 41118 agggagctattcatgccaagtacgatgcaattgataaagacactccaattcctacagata 41059
```

5)

```
Query: 1508  gacaa 1512
              |||||
Sbjct: 41058 gacaa 41054
```

Score = 129 bits (65), Expect = 1e-26
Identities = 65/65 (100%)
Strand = Plus / Minus

```
Query: 719   aggagcttcctgaaactgtgatagatcttttgaataagtgccttaccttccatccttcta 778
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 55774 aggagcttcctgaaactgtgatagatcttttgaataagtgccttaccttccatccttcta 55715
```

6)

```
Query: 779   agagg 783
              |||||
Sbjct: 55714 agagg 55710
```

Score = 127 bits (64), Expect = 4e-26
Identities = 64/64 (100%)
Strand = Plus / Minus

```
Query: 658   gattgtgtagatgacactttaatagttctggctgaagagcatggttgtttggacattata 717
```

7)

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 56449 gattgtgtagatgacactttaatagttctggctgaagagcatggttgtttggacattata 56390


Query: 718   aagg 721
            ||||
Sbjct: 56389 aagg 56386
```

Score = 123 bits (62), Expect = 6e-25
Identities = 62/62 (100%)
Strand = Plus / Minus

```
Query: 597   gggaagaaaattatttcagagcttggatatttctgaaagactaaaatttttgcttacttt 656
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 57945 gggaagaaaattatttcagagcttggatatttctgaaagactaaaatttttgcttacttt 57886
```

6

```
Query: 657   gg 658
            ||
Sbjct: 57885 gg 57884
```

Score = 105 bits (53), Expect = 1e-19
Identities = 53/53 (100%)
Strand = Plus / Minus

7

```
Query: 1638  aggtcttgactcactttgtgctccattcctatatctaaacttcaataatgaag 1690
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 39247 aggtcttgactcactttgtgctccattcctatatctaaacttcaataatgaag 39195
```

Score = 99.6 bits (50), Expect = 9e-18
Identities = 50/50 (100%)
Strand = Plus / Minus

8

```
Query: 1171  agattgaaagatgttggtggagaagcattttacccattacttgaagatga 1220
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 44274 agattgaaagatgttggtggagaagcattttacccattacttgaagatga 44225
```

Score = 73.8 bits (37), Expect = 5e-10
Identities = 37/37 (100%)
Strand = Plus / Minus

9

```
Query: 1861 ctctatgccatcccttggtttcttaccatgtttactc 1897
            |||||||||||||||||||||||||||||||||||||
Sbjct: 2220 ctctatgccatcccttggtttcttaccatgtttactc 2184


>AP001820.2.1.101947
```

```
          Length = 101947

 Score =  224 bits (113), Expect = 2e-55
 Identities = 113/113 (100%)
 Strand = Plus / Plus


Query: 2570  agtttgcagctcaccttgtgaagatgaaatatccaagaatctgtattctagatggtggca 2629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 26799 agtttgcagctcaccttgtgaagatgaaatatccaagaatctgtattctagatggtggca 26858


Query: 2630  ttaataaaataaagccaacaggcctcctcaccatcccatctcctcaaatatga 2682
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 26859 ttaataaaataaagccaacaggcctcctcaccatcccatctcctcaaatatga 26911



>AC109361.4.1.133749
          Length = 133749

 Score =  224 bits (113), Expect = 2e-55
 Identities = 113/113 (100%)
 Strand = Plus / Minus


Query: 2570   agtttgcagctcaccttgtgaagatgaaatatccaagaatctgtattctagatggtggca 2629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 124356 agtttgcagctcaccttgtgaagatgaaatatccaagaatctgtattctagatggtggca 124297


Query: 2630   ttaataaaataaagccaacaggcctcctcaccatcccatctcctcaaatatga 2682
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 124296 ttaataaaataaagccaacaggcctcctcaccatcccatctcctcaaatatga 124244


  Database: Homo_sapiens.latestgp.fa
    Posted date:  Jul 8, 2003 12:51 PM
  Number of letters in database: 200,800,637,119
  Number of sequences in database:  26,679

Lambda     K      H
    1.37    0.711     1.31

Gapped
Lambda     K      H
    1.37    0.711     1.31


Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 0, Extension: 0
Number of Hits to DB: 0
length of query: 5366
length of database: 200,800,637,119
effective HSP length: 22
effective length of query: 2660
effective search space used:        0
T: 0
A: 0
```

```
X1: 0 ( 0.0 bits)
X2: 20 (39.6 bits)
S1: 12 (24.3 bits)
S2: 24 (48.1 bits)
```